NCBI

Search Nucleotide ▼ for [   ] Go   Clear

Limits   Preview/Index   History   Clipboard   Details

Display default ▼ Show: 20 ▼   Send to File ▼   Get Subsequence

☐ **1**: NM_074070. Caenorhabditis el...[gi:17563083]   Links

```
LOCUS       5O445Co                 738 bp    mRNA    linear   INV 22-NOV-2002
DEFINITION  Caenorhabditis elegans GYF domain containing protein (27.5 kD),
            alternative variant d, mRNA.
ACCESSION   NM_074070
VERSION     NM_074070.1  GI:17563083
KEYWORDS    .
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
COMMENT     VALIDATED REFSEQ: This record has undergone preliminary review of
            the sequence, but has not yet been subject to final NCBI review.
            The reference sequence was derived from WormBase CDS:R10D12.14.
            Fully supported by cDNA from the Worm Transcriptome Project.
            COMPLETENESS: full length.
FEATURES             Location/Qualifiers
     source          1..738
                     /organism="Caenorhabditis elegans"
                     /db_xref="taxon:6239"
                     /chromosome="V"
                     /map="V;+5.72 cM (interpolated genetic position)"
                     /map="V; covering 3369 bp, from base 13965013 to 13968383
                     on genome release WS85"
                     /clone="Primers to amplify the CDS (Stop included):
                     ATGCACAAGAACGGAAACAATGGA (T=58.5),
                     TTAGTTGATGATAACCATTTGTCCGAG (T=59.0)"
                     /clone_lib="[Predicted cellular localisation] PSORT II
                     analysis, (K. Nakai) trained on yeast data predicts that
                     the subcellular location of this protein is most likely in
                     the nucleus (56%). Less likely possibilities are in the
                     cytoplasm (26%) or in the cytoskeleton (13%) or in the
                     mitochondria (4%)."
     gene            1..738
                     /gene="5O445Co"
                     /note="50445; synonyms: R10D12.13a, R10D12.13b,
                     R10D12.13c, R10D12.14, CELK02289"
     CDS             1..738
                     /gene="5O445Co"
                     /note="|| [Common ancestor, from TaxBlast with threshold
                     10-3] Fungi Metazoa group  || [Closest homologs]
                     Schizosaccharomyces pombe: ref|NP 594756.1| (score=45);
                     Caenorhabditis elegans: ref|NP 506471.1| (422); Drosophila
                     melanogaster: gb|AAF59406.1| (46); Mus musculus: ref|NP
                     113596.1| (49); Homo sapiens: dbj|BAA91873.1| (50)"
                     /codon_start=1
                     /product="GYF domain containing protein (27.5 kD)"
                     /protein_id="NP_506471.1"
```

h   cb   hg e e   e fcg c   e e   b   ce   e

```
                    /db_xref="GI:17563084"
                    /db_xref="AceView/WormGenes:50445Co"
                    /db_xref="CDD:pfam02213"
                    /db_xref="LocusID:179891"
                    /db_xref="NextDB:CELK02289"
                    /db_xref="WorfDB:R10D12.13a"
                    /db_xref="WormBase:R10D12.13a"
                    /db_xref="WormBase:R10D12.13b"
                    /db_xref="WormBase:R10D12.13c"
                    /db_xref="WormBase:R10D12.14"
                    /translation="MHKNGNNGPVIDTKWHYLGPDSEKYGPYMSKDMLFWLQAGYFND
                    GLQLKTENEPNYHTLGEWSQLLGTHPFSMPVHSLDATIAQMNSMRPHGAMMMVPPGLQ
                    NQFQPPMPMRFPPFLPMPLLHQMNQNGPPMGAQMHSQPPSEPIDAGSLSHTPDSENET
                    RLNEQTLQQPPSWLIALGLAGHGRKPHHHQQILAHQHIPQMQHANVATDQVVMKSVEC
                    QTEPVEISKEQASRVLSELLGQMVIIN"
     misc_feature   37..204
                    /gene="50445Co"
                    /note="Region: [Pfam/InterPro description] GYF domain: the
                    GYF domain is named because of the presence of Gly-Tyr-Phe
                    residues. The GYF domain is a proline-binding domain in
                    CD2-binding protein O95400. HMMER score 38.20
                    Evalue=1.2e-08"
                    /db_xref="CDD:pfam02213"
BASE COUNT        211 a      204 c      159 g      164 t
ORIGIN
        1 atgcacaaga acggaaacaa tggacctgtc attgacacaa aatggcacta tctcggccct
       61 gacagtgaaa aatatggacc atatatgtca aaggatatgc tgttctggct tcaagcggga
      121 tacttcaacg acggtctcca attgaaaact gaaaatgagc caaactatca tacgcttgga
      181 gagtggagcc aattgctcgg aactcaccca ttcagtatgc ctgtgcactc actggatgcg
      241 acgattgctc agatgaactc aatgcggcct cacggagcaa tgatgatggt tccacctgga
      301 cttcaaaatc aattccaacc accgatgccg atgcgtttcc caccattcct tccaatgccg
      361 cttctccatc aaatgaatca aaatggacca ccaatgggtg ctcaaatgca ttctcagcca
      421 ccatcggagc caatcgacgc tggatctctg tcccataccc cagattccga gaacgaaacg
      481 cggttaaacg agcaaactct ccagcagcct ccatcgtggc taattgccct tggcctggcg
      541 ggacatggtc gtaagccaca ccatcatcag caaattcttg cccatcagca catcccacag
      601 atgcagcacg ctaatgttgc caccgaccaa gttgtgatga agagcgtcga gtgccagaca
      661 gagccagttg agatttcaaa ggaacaggct tctcgtgttc tttccgagtt gctcggacaa
      721 atggttatca tcaactaa
//
```

Jan 21 2003 18:08:12

h   cb   hg e   e   e fcg c   e   e   b   c e   e